

*Dwight*

SEQUENCE LISTING

<110> Lawn, Richard M.  
Wade, David  
Garvin, Michael

<120> Compositions and Methods for Increasing Cholesterol Efflux and Raising HDL using ATP Binding Cassette Transporter Protein ABC1

<130> 99,395-B

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<150> US 60/140,264

<151> 1999-06-18

<150> US 60/153,872

<151> 1999-08-14

<150> US 60/166,573

<151> 1999-11-19

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<170> PatentIn Ver. 2.0

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DEPARTMENT OF GENETICS

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Leu Phe Ile Phe Leu Ile Leu Ile Ser Val Arg Leu Ser Tyr Pro Pro  
35 40 45

Tyr Glu Gln His Glu Cys His Phe Pro Asn Lys Ala Met Pro Ser Ala  
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Gly Thr Leu Pro Trp Val Gln Gly Ile Ile Cys Asn Ala Asn Asn Pro  
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Cys Phe Arg Tyr Pro Thr Pro Gly Glu Ala Pro Gly Val Val Gly Asn  
85 90 95

Phe Asn Lys Ser Ile Val Ala Arg Leu Phe Ser Asp Ala Arg Arg Leu  
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Leu Leu Tyr Ser Gln Lys Asp Thr Ser Met Lys Asp Met Arg Lys Val  
115 120 125

Leu Arg Thr Leu Gln Gln Ile Lys Lys Ser Ser Ser Asn Leu Lys Leu  
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Gln Asp Phe Leu Val Asp Asn Glu Thr Phe Ser Gly Phe Leu Tyr His  
145 150 155 160

Asn Leu Ser Leu Pro Lys Ser Thr Val Asp Lys Met Leu Arg Ala Asp  
165 170 175

Val Ile Leu His Lys Val Phe Leu Gln Gly Tyr Gln Leu His Leu Thr  
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Ser Leu Cys Asn Gly Ser Lys Ser Glu Glu Met Ile Gln Leu Gly Asp  
195 200 205

Gln Glu Val Ser Glu Leu Cys Gly Leu Pro Lys Glu Lys Leu Ala Ala  
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Ala Glu Arg Val Leu Arg Ser Asn Met Asp Ile Leu Lys Pro Ile Leu  
225 230 235 240

Arg Thr Leu Asn Ser Thr Ser Pro Phe Pro Ser Lys Glu Leu Ala Glu  
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Ala Thr Lys Thr Leu Leu His Ser Leu Gly Thr Leu Ala Gln Glu Leu  
260 265 270

Phe Ser Met Arg Ser Trp Ser Asp Met Arg Gln Glu Val Met Phe Leu  
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Thr Asn Val Asn Ser Ser Ser Ser Thr Gln Ile Tyr Gln Ala Val  
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Ser Arg Ile Val Cys Gly His Pro Glu Gly Gly Leu Lys Ile Lys  
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Ser Leu Asn Trp Tyr Glu Asp Asn Asn Tyr Lys Ala Leu Phe Gly Gly  
325 330 335

Asn Gly Thr Glu Glu Asp Ala Glu Thr Phe Tyr Asp Asn Ser Thr Thr  
340 345 350

Pro Tyr Cys Asn Asp Leu Met Lys Asn Leu Glu Ser Ser Pro Leu Ser  
355 360 365

Arg Ile Ile Trp Lys Ala Leu Lys Pro Leu Leu Val Gly Lys Ile Leu  
370 375 380

Tyr Thr Pro Asp Thr Pro Ala Thr Arg Gln Val Met Ala Glu Val Asn  
385 390 395 400

Lys Thr Phe Gln Glu Leu Ala Val Phe His Asp Leu Glu Gly Met Trp  
405 410 415

Glu Glu Leu Ser Pro Lys Ile Trp Thr Phe Met Glu Asn Ser Gln Glu  
420 425 430

Met Asp Leu Val Arg Met Leu Leu Asp Ser Arg Asp Asn Asp His Phe  
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Trp Glu Gln Gln Leu Asp Gly Leu Asp Trp Thr Ala Gln Asp Ile Val  
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Ala Phe Leu Ala Lys His Pro Glu Asp Val Gln Ser Ser Asn Gly Ser  
465 470 475 480

Val Tyr Thr Trp Arg Glu Ala Phe Asn Glu Thr Asn Gln Ala Ile Arg  
485 490 495

Thr Ile Ser Arg Phe Met Glu Cys Val Asn Leu Asn Lys Leu Glu Pro  
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Ile Ala Thr Glu Val Trp Leu Ile Asn Lys Ser Met Glu Leu Leu Asp  
515 520 525

Glu Arg Lys Phe Trp Ala Gly Ile Val Phe Thr Gly Ile Thr Pro Gly  
530 535 540

Ser Ile Glu Leu Pro His His Val Lys Tyr Lys Ile Arg Met Asp Ile  
545 550 555 560

Asp Asn Val Glu Arg Thr Asn Lys Ile Lys Asp Gly Tyr Trp Asp Pro  
565 570 575

Gly Pro Arg Ala Asp Pro Phe Glu Asp Met Trp Tyr Val Trp Gly Gly  
580 585 590

Phe Ala Tyr Leu Gln Asp Val Val Glu Gln Ala Ile Ile Arg Val Leu  
595 600 605

Thr Gly Thr Glu Lys Lys Thr Gly Val Tyr Met Gln Gln Met Pro Tyr  
610 615 620

Pro Cys Tyr Val Asp Asp Ile Phe Leu Arg Val Met Ser Arg Ser Met  
625 630 635 640

Pro Leu Phe Met Thr Leu Ala Trp Ile Tyr Ser Val Ala Val Ile Ile  
645 650 655

DESIGNER: GENE

Lys Gly Ile Val Tyr Glu Lys Glu Ala Arg Leu Lys Glu Thr Met Arg  
660 665 670

Ile Met Gly Leu Asp Asn Ser Ile Leu Trp Phe Ser Trp Phe Ile Ser  
675 680 685

Ser Leu Ile Pro Leu Leu Val Ser Ala Gly Leu Leu Val Val Ile Leu  
690 695 700

Lys Leu Gly Asn Leu Leu Pro Tyr Ser Asp Pro Ser Val Val Phe Val  
705 710 715 720

Phe Leu Ser Val Phe Ala Val Val Thr Ile Leu Gln Cys Phe Leu Ile  
725 730 735

Ser Thr Leu Phe Ser Arg Ala Asn Leu Ala Ala Ala Cys Gly Gly Ile  
740 745 750

Ile Tyr Phe Thr Leu Tyr Leu Pro Tyr Val Leu Cys Val Ala Trp Gln  
755 760 765

Asp Tyr Val Gly Phe Thr Leu Lys Ile Phe Ala Ser Leu Leu Ser Pro  
770 775 780

Val Ala Phe Gly Phe Gly Cys Glu Tyr Phe Ala Leu Phe Glu Glu Gln  
785 790 795 800

Gly Ile Gly Val Gln Trp Asp Asn Leu Phe Glu Ser Pro Val Glu Glu  
805 810 815

Asp Gly Phe Asn Leu Thr Thr Ser Ile Ser Met Met Leu Phe Asp Thr  
820 825 830

Phe Leu Tyr Gly Val Met Thr Trp Tyr Ile Glu Ala Val Phe Pro Gly  
835 840 845

Gln Tyr Gly Ile Pro Arg Pro Trp Tyr Phe Pro Cys Thr Lys Ser Tyr  
850 855 860

Trp Phe Gly Glu Glu Ser Asp Glu Lys Ser His Pro Gly Ser Asn Gln  
865 870 875 880

Lys Arg Met Ser Glu Ile Cys Met Glu Glu Glu Pro Thr His Leu Lys  
885 890 895

Leu Gly Val Ser Ile Gln Asn Leu Val Lys Val Tyr Arg Asp Gly Met  
900 905 910

Lys Val Ala Val Asp Gly Leu Ala Leu Asn Phe Tyr Glu Gly Gln Ile  
915 920 925

Thr Ser Phe Leu Gly His Asn Gly Ala Gly Lys Thr Thr Thr Met Ser  
930 935 940

Ile Leu Thr Gly Leu Phe Pro Pro Thr Ser Gly Thr Ala Tyr Ile Leu  
945 950 955 960

Gly Lys Asp Ile Arg Ser Glu Met Ser Thr Ile Arg Gln Asn Leu Gly  
965 970 975

Val Cys Pro Gln His Asn Val Leu Phe Asp Met Leu Thr Val Glu Glu  
980 985 990

His Ile Trp Phe Tyr Ala Arg Leu Lys Gly Leu Ser Glu Lys His Val  
995 1000 1005

Lys Ala Glu Met Glu Gln Met Ala Leu Asp Val Gly Leu Pro Ser Ser  
1010 1015 1020

Lys Leu Lys Ser Lys Thr Ser Gln Leu Ser Gly Gly Met Gln Arg Lys  
1025 1030 1035 1040

Leu Ser Val Ala Leu Ala Phe Val Gly Gly Ser Lys Val Val Ile Leu  
1045 1050 1055

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1060 1065 1070

Glu Leu Leu Leu Lys Tyr Arg Gln Gly Arg Thr Ile Ile Leu Ser Thr  
1075 1080 1085

His His Met Asp Glu Ala Asp Val Leu Gly Asp Arg Ile Ala Ile Ile  
1090 1095 1100

Ser His Gly Lys Leu Cys Cys Val Gly Ser Ser Leu Phe Leu Lys Asn  
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Gln Leu Gly Thr Gly Tyr Tyr Leu Thr Leu Val Lys Lys Asp Val Glu  
1125 1130 1135

Ser Ser Leu Ser Ser Cys Arg Asn Ser Ser Ser Thr Val Ser Tyr Leu  
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Lys Lys Glu Asp Ser Val Ser Gln Ser Ser Ser Asp Ala Gly Leu Gly  
1155 1160 1165

Ser Asp His Glu Ser Asp Thr Leu Thr Ile Asp Val Ser Ala Ile Ser  
1170 1175 1180

Asn Leu Ile Arg Lys His Val Ser Glu Ala Arg Leu Val Glu Asp Ile  
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Gly His Glu Leu Thr Tyr Val Leu Pro Tyr Glu Ala Ala Lys Glu Gly  
1205 1210 1215

Ala Phe Val Glu Leu Phe His Glu Ile Asp Asp Arg Leu Ser Asp Leu  
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Gly Ile Ser Ser Tyr Gly Ile Ser Glu Thr Thr Leu Glu Glu Ile Phe  
1235 1240 1245

Leu Lys Val Ala Glu Glu Ser Gly Val Asp Ala Glu Thr Ser Asp Gly  
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Cys Leu Arg Pro Phe Thr Glu Asp Asp Ala Ala Asp Pro Asn Asp Ser  
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Gly Lys Gly Ser Tyr Gln Val Lys Gly Trp Lys Leu Thr Gln Gln Gln  
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Phe Val Ala Leu Leu Trp Lys Arg Leu Leu Ile Ala Arg Arg Ser Arg  
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Lys Gly Phe Phe Ala Gln Ile Val Leu Pro Ala Val Phe Val Cys Ile  
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Ala Leu Val Phe Ser Leu Ile Val Pro Pro Phe Gly Lys Tyr Pro Ser  
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Pro Asp Thr Pro Cys Gln Ala Gly Glu Glu Trp Thr Thr Ala Pro  
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Val Pro Gln Thr Ile Met Asp Leu Phe Gln Asn Gly Asn Trp Thr Met  
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Gln Asn Pro Ser Pro Ala Cys Gln Cys Ser Ser Asp Lys Ile Lys Lys  
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Met Leu Pro Val Cys Pro Pro Gly Ala Gly Gly Leu Pro Pro Pro Gln  
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Arg Lys Gln Asn Thr Ala Asp Ile Leu Gln Asp Leu Thr Gly Arg Asn  
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Leu Gly Val Ser Asn Thr Gln Ala Leu Pro Pro Ser Gln Glu Val Asn  
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Asp Ala Ile Lys Gln Met Lys Lys His Leu Lys Leu Ala Lys Asp Ser  
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Ser Ala Asp Arg Phe Leu Asn Ser Leu Gly Arg Phe Met Thr Gly Leu  
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Asp Thr Arg Asn Asn Val Lys Val Trp Phe Asn Asn Lys Gly Trp His  
1585 1590 1595 1600

Ala Ile Ser Ser Phe Leu Asn Val Ile Asn Asn Ala Ile Leu Arg Ala  
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Asn Leu Gln Lys Gly Glu Asn Pro Ser His Tyr Gly Ile Thr Ala Phe  
1620 1625 1630

Asn His Pro Leu Asn Leu Thr Lys Gln Gln Leu Ser Glu Val Ala Leu  
1635 1640 1645

Met Thr Thr Ser Val Asp Val Leu Val Ser Ile Cys Val Ile Phe Ala  
1650 1655 1660

Met Ser Phe Val Pro Ala Ser Phe Val Val Phe Leu Ile Gln Glu Arg  
1665 1670 1675 1680

Val Ser Lys Ala Lys His Leu Gln Phe Ile Ser Gly Val Lys Pro Val  
1685 1690 1695

Ile Tyr Trp Leu Ser Asn Phe Val Trp Asp Met Cys Asn Tyr Val Val  
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Pro Ala Thr Leu Val Ile Ile Phe Ile Cys Phe Gln Gln Lys Ser  
1715 1720 1725

Tyr Val Ser Ser Thr Asn Leu Pro Val Leu Ala Leu Leu Leu Leu  
1730 1735 1740

Tyr Gly Trp Ser Ile Thr Pro Leu Met Tyr Pro Ala Ser Phe Val Phe  
1745 1750 1755 1760

Lys Ile Pro Ser Thr Ala Tyr Val Val Leu Thr Ser Val Asn Leu Phe  
1765 1770 1775

Ile Gly Ile Asn Gly Ser Val Ala Thr Phe Val Leu Glu Leu Phe Thr  
1780 1785 1790

Asp Asn Lys Leu Asn Asn Ile Asn Asp Ile Leu Lys Ser Val Phe Leu  
1795 1800 1805

Ile Phe Pro His Phe Cys Leu Gly Arg Gly Leu Ile Asp Met Val Lys  
1810 1815 1820

Asn Gln Ala Met Ala Asp Ala Leu Glu Arg Phe Gly Glu Asn Arg Phe  
1825 1830 1835 1840

Val Ser Pro Leu Ser Trp Asp Leu Val Gly Arg Asn Leu Phe Ala Met  
1845 1850 1855

Ala Val Glu Gly Val Val Phe Phe Leu Ile Thr Val Leu Ile Gln Tyr  
1860 1865 1870

Arg Phe Phe Ile Arg Pro Arg Pro Val Asn Ala Lys Leu Ser Pro Leu  
1875 1880 1885

Asn Asp Glu Asp Glu Asp Val Arg Arg Glu Arg Gln Arg Ile Leu Asp  
1890 1895 1900

Gly Gly Gly Gln Asn Asp Ile Leu Glu Ile Lys Glu Leu Thr Lys Ile  
1905 1910 1915 1920

Tyr Arg Arg Lys Arg Lys Pro Ala Val Asp Arg Ile Cys Val Gly Ile  
1925 1930 1935

Pro Pro Gly Glu Cys Phe Gly Leu Leu Gly Val Asn Gly Ala Gly Lys  
1940 1945 1950

Ser Ser Thr Phe Lys Met Leu Thr Gly Asp Thr Thr Val Thr Arg Gly  
1955 1960 1965

Asp Ala Phe Leu Asn Lys Asn Ser Ile Leu Ser Asn Ile His Glu Val  
1970 1975 1980

His Gln Asn Met Gly Tyr Cys Pro Gln Phe Asp Ala Ile Thr Glu Leu  
1985 1990 1995 2000

Leu Thr Gly Arg Glu His Val Glu Phe Phe Ala Leu Leu Arg Gly Val  
2005 2010 2015

Pro Glu Lys Glu Val Gly Lys Val Gly Glu Trp Ala Ile Arg Lys Leu  
2020 2025 2030

Gly Leu Val Lys Tyr Gly Glu Lys Tyr Ala Gly Asn Tyr Ser Gly Gly  
2035 2040 2045

Asn Lys Arg Lys Leu Ser Thr Ala Met Ala Leu Ile Gly Gly Pro Pro  
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Val Val Phe Leu Asp Glu Pro Thr Thr Gly Met Asp Pro Lys Ala Arg  
2065 2070 2075 2080

Arg Phe Leu Trp Asn Cys Ala Leu Ser Val Val Lys Glu Gly Arg Ser  
2085 2090 2095

Val Val Leu Thr Ser His Ser Met Glu Glu Cys Glu Ala Leu Cys Thr  
2100 2105 2110

Arg Met Ala Ile Met Val Asn Gly Arg Phe Arg Cys Leu Gly Ser Val  
2115 2120 2125

Gln His Leu Lys Asn Arg Phe Gly Asp Gly Tyr Thr Ile Val Val Arg  
2130 2135 2140

Ile Ala Gly Ser Asn Pro Asp Leu Lys Pro Val Gln Asp Phe Phe Gly  
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Leu Ala Phe Pro Gly Ser Val Leu Lys Glu Lys His Arg Asn Met Leu  
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Gln Tyr Gln Leu Pro Ser Ser Leu Ser Ser Leu Ala Arg Ile Phe Ser  
2180 2185 2190

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2210 2215 2220

Ser Asp Asp Asp His Leu Lys Asp Leu Ser Leu His Lys Asn Gln Thr  
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amplification primer

<400> 12  
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<210> 13  
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DRAFT GENOME

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<210> 32  
<211> 18  
<212> DNA  
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<220>

<220>  
<223> Description of Artificial Sequence: ABC1 sequencing primer

<400> 32  
tttttcctca ttactgtt 18

<210> 33  
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<212> DNA

18

<213> Artificial Sequence

<220>

<220>

<223> Description of Artificial Sequence: ABC1 sequencing primer

<400> 33

gatgccatca cagagctg

<210> 34

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<220>

<223> Description of Artificial Sequence: ABC1 sequencing primer

<400> 34

agtgtccagc atctaaa

17

<210> 35

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<220>

<223> Description of Artificial Sequence: ABC1 sequencing primer

<400> 35

caaagttcac aaatactt

18

<210> 36

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<220>

<223> Description of Artificial Sequence: ABC1

DNA Sequence Database

sequencing primer

<400> 36  
cttagggcac aattccaca 19

<210> 37  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<220>  
<223> Description of Artificial Sequence: ABC1  
sequencing primer

<400> 37  
tgaaagttga tgatttc 18

<210> 38  
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<212> DNA  
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<223> Description of Artificial Sequence: ABC1  
sequencing primer

<400> 38  
ttttcacca tgtcgatga 19

<210> 39  
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<213> Artificial Sequence

<220>

<220>  
<223> Description of Artificial Sequence: ABC1  
sequencing primer

<400> 39  
ctccactgat gaactgc 17

<210> 40

DRAFT - USE WITH CARE

<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<220>  
<223> Description of Artificial Sequence: ABC1 sequencing primer

<400> 40  
gtttcttcat ttgtttga 18

<210> 41  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

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<223> Description of Artificial Sequence: ABC1 sequencing primer

<400> 41  
agggcgtgtc tgggattg 18

<210> 42  
<211> 18  
<212> DNA  
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<223> Description of Artificial Sequence: ABC1 sequencing primer

<400> 42  
cagaatcatt tggatcag 18

<210> 43  
<211> 18  
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<213> Artificial Sequence

<220>

SEQUENCE LISTING

<220>  
<223> Description of Artificial Sequence: ABC1  
sequencing primer

<400> 43  
catcagaact gctctgag  
  
<210> 44  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>

<220>  
<223> Description of Artificial Sequence: ABC1  
sequencing primer

<400> 44  
agctggcttg ttttgcttt  
  
<210> 45  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<220>  
<223> Description of Artificial Sequence: ABC1  
sequencing primer

<400> 45  
tggacacgccc cagcttca  
  
<210> 46  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<220>  
<223> Description of Artificial Sequence: ABC1  
sequencing primer

<400> 46  
cctgccatgc cacacaca

18

19

18

18

DNA SEQUENCING

<210> 47  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<220>  
<223> Description of Artificial Sequence: ABC1  
sequencing primer

<400> 47  
ctcatcaccc gcagaaaag 18

<210> 48  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<220>  
<223> Description of Artificial Sequence: ABC1  
sequencing primer

<400> 48  
cacactccat gaagcgag 18

<210> 49  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>

<220>  
<223> Description of Artificial Sequence: ABC1  
sequencing primer

<400> 49  
tccagataat gcggggaaa 18

<210> 50  
<211> 18  
<212> DNA  
<213> Artificial Sequence

0  
1  
2  
3  
4  
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6  
7  
8  
9

<220>

<220>

<223> Description of Artificial Sequence: ABC1 sequencing primer

<400> 50 tcaggattgg cttcagga 18

<210> 51

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<220>

<223> Description of Artificial Sequence: ABC1 sequencing primer

<400> 51 aagtttgagc tggatttctt g 21

<210> 52

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<220>

<223> Description of Artificial Sequence: beta-globin antisense oligonucleotide

<400> 52 cctcttacct cagttacaat ttata 25

<210> 53

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<220>

<223> Description of Artificial Sequence: ABC1 antisense oligonucleotide

DRAFT GENOME

<400> 53  
catgttgttc atagggtggg tagctc 26

<210> 54  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<220>  
<223> Description of Artificial Sequence: beta-actin amplification primer

<400> 54  
tcacccacac tgtgccatct acga 24

<210> 55  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>

<220>  
<223> Description of Artificial Sequence: beta-actin amplification primer

<400> 55  
cagcggaacc gtcattgcc aatgg 25

<210> 56  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>

<220>  
<223> Description of Artificial Sequence: sterol response element oligonucleotide

<400> 56  
tcgagtgacc gatagtaacc tctcga 26

<210> 57  
<211> 26  
<212> DNA

*Artificial*

<213> Artificial Sequence

<220>

<220>

<223> Description of Artificial Sequence: mutated sterol  
response element oligonucleotide

<400> 57

tcgagctgca catagtaacc tctcga

26

O E S S E C H T " O C E A E G C